

```

MORK1 MESPIQIFRGDPGPTCSACLLPNSSW:::FPNWAESDSNGSVGEDQQLESAHISPAIVITAVY    TM1
**      *** |** ** * ** * *| ***|*
MORD1 ME::::::::::LVPSARAELOQSSPLVNLSDAFPSAFPAGANASGPSARSASSL:::ALAIATILY
TM2
MORK1 SVFVVGLVGNSLVMFVIIRYTKMTATNIYIFNALADALVTTPFQSAVYLMSWPFGDVLCKIVISID
* * ***|** **** *|****|***** *|***** *** |***|*** *|***
MORD1 SAVCAVGLGNVLVMFEGIVRYTKLTATNIYIFNALADALATSTLPFQSAKYLMETWPFGEKLLCKAVLSID
TM3          TM 4
MORK1 YYNMFTSIFTLTMMSVDRIYAUCHPVKALDFRTPAKAKIINICIWLASSVGISAIVLGGTKVREDVDVIEC
*****
MORD1 YYNMFTSIFTLTMMSVDRIYAUCHPVKALDFRTPAKAKLINICIWLASGVGPIMVMAVTQPRDGAVV::C
TM 5
MORK1 SLOFPDEYSWDLFMKICVFVFAFVIPVLIIVCYTLMILRLKSVRLLSGSREKDRNLRRITKLVLVVAV
**** | ** *****|****|*|*** ** **|***|*****|**** *****|*****
MORD1 MLQFPSPSW:YWDVTVKICVFLFAFVVPILIITVCYGLMLRLRSVRLLSGSKEKDRSLRRITRMVLVVUGA
TM 6          TM 7
MORK1 FIICWTPIHIFILVEALGSTSHSTAALSSYY:FCIALGYTNSSLNPVL YAFLDENFKRCFRDFCFPIKMRME
*||** *****||* * | ***** *****
MORD1 FWCWAPIHIFIVWTLVDINRRDPLVVAALHLCIALGYANSSNPVL YAFLDENFKRCFRQLCRTPCGRQE
MORK1 RQSTNRVRNTVQDP:::ASMRDVGGMNKPV 380 (SEQ ID NO:2)
* * *| | * *
MORD1 PGSRLRRPQATTREVRTACTPSDGGGAAA 372 (SEQ ID NO:4)

```

FIG. 1

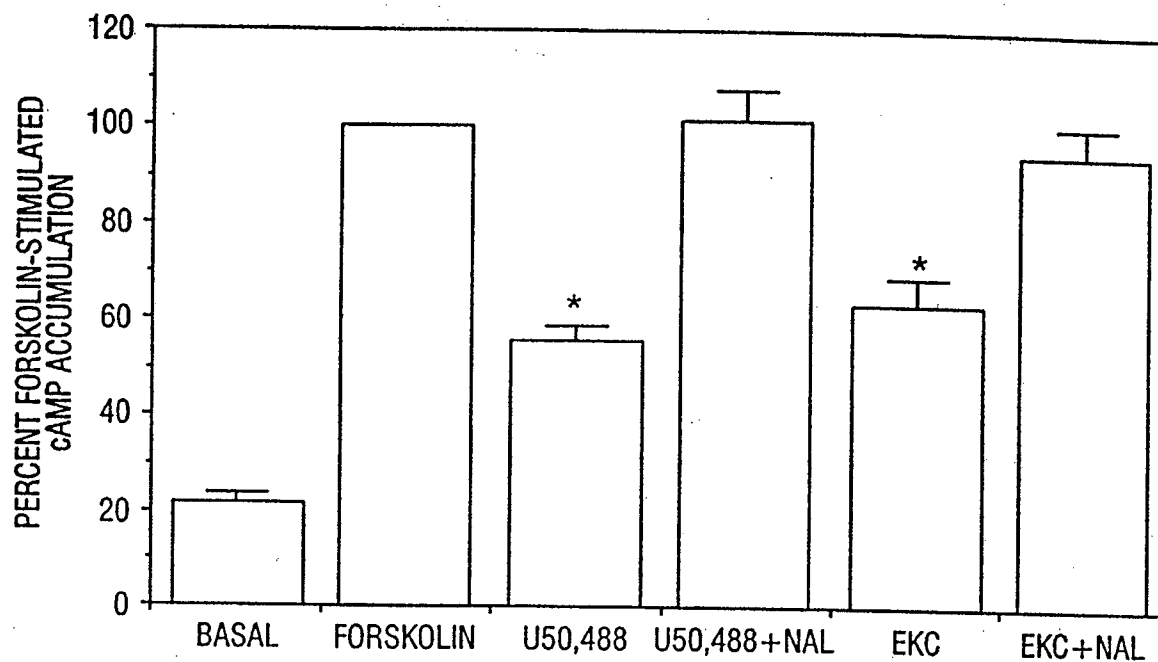


FIG. 2A

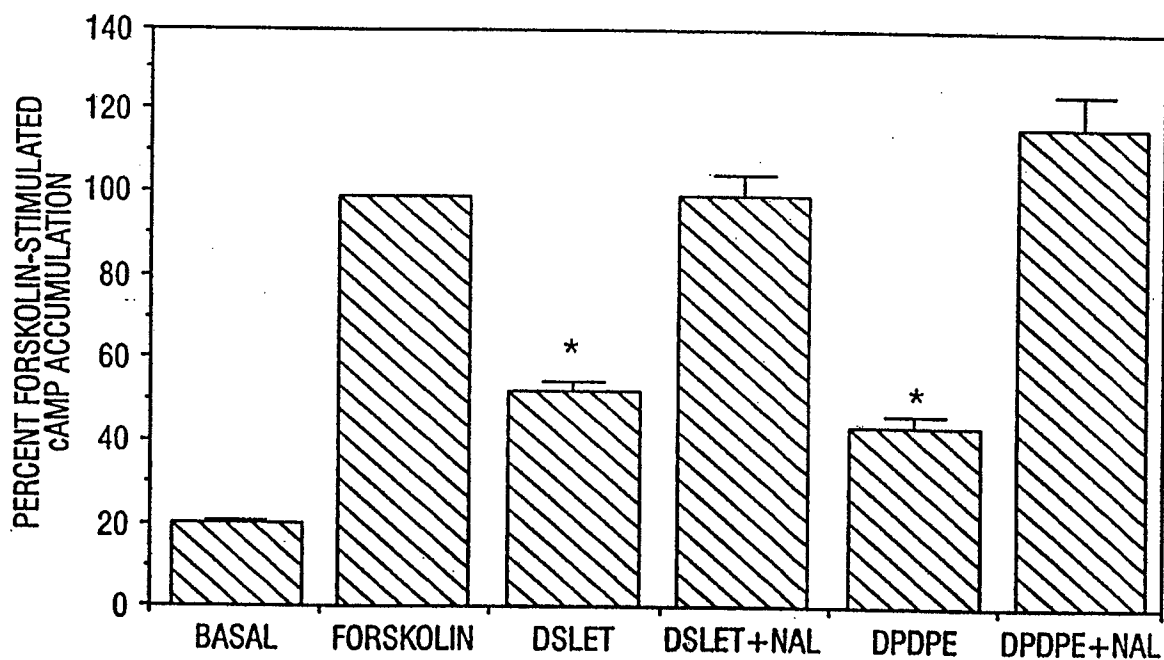


FIG. 2B

REPLACEMENT
SHEET

1	AAGAAGCAAATCAGTAATCCAAGGCTATCACAAACACATTACCTTATGGGGTTTGAC	
61	TTGAAAATGGAGGGAATGCTATTGTTTCTTTTCTTTTAGATACACAAAGATGAAGACAG	TyrThrLysMetLysThrAla
121	ThrAsnIleTyrIlePheAsnLeuAlaLeuAlaAspAlaLeuValThrThrThrMetPro CAACCAACATTTACATAATTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGC	
181	PheGlnSerThrValTyrLeuMetAsnSerTrpProPheGlyAspValLeuCysLysIle CCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTTGGGGATGTGCTGTGCAAGA	
241	ValIleSerIleAspTyrTyrAsnMetPheThrSerIlePheThrLeuThrMetMetSer TAGTAATTTCCATTGATTACTACAACATGTTACCAGCATCTTCACCTTGACCATGATGA	
301	ValAspArgTyrIleAlaValCysHisProValLysAlaLeuAspPheArgThrProLeu GCGTGGACCGCTACATTGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCT	
361	LysAlaLysIleIleAsnIleCysIleTrpLeuLeuSerSerSerValGlyIleSerAla TGAAGGCAAAGATCATCAATATCTGCATCTGGCTGCTGTGTCATCTGTGGCATCTCTG	

FIG. 3A

LysAlaLysIleIleAsnIleCysIleTrpLeuLeuSerSerValGlyIleSerAla
361 TGAAGGCAAAGATCATCAATATCTGCATCTGGCTGCTGCTCATCTGTTGGCATCTCTG

IleValLeuGlyGlyThrLysValArgGluA
421 CAATAGTCCTTGGAGGCACCAAGTCAGGGAAGGT:.....:TTTCTGTGTTGT

spValAspValIleGluCysCysLeuGlnPheProAsp
481 GGTTTTTATTGCCCTCCTCCAGACGTCGATGTCAATTGAGTGCTGCTTGCAGTTCCCAGAT

AspAspTyrSerTrpTrpAspLeuPheMetLysIleCysValPheIlePheAlaPheVal
541 GATGACTACTCCTGGTGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCCTTCGTG

IleProValLeuIleIleValCysTyrThrLeuMetIleLeuArgLeuLysNNNVal
601 ATCCCTGTCCCTCATCATCATCGTCTGCTACACCTGATGATCCTGCGTCTCAAGANNGTC

ArgLeuLeuSerGlySerArgGluLysAspNNNAsnLeuArgArgIleThrArgLeuVal
661 CGGCTCCTTTCTGGCTCCCGAGAGAAAGATNNCAACCTGCGTAGGATCACCAAGACTGGTC

FIG. 3B

REPLACEMENT
SHEET

661	ArgLeuLeuSerGlySerArgGluLysAspNNNAsnLeuArgArgIleThrArgLeuVal CGGCTCCTTTCTGGCTCCGAGAGAAAGATNNCAACCTGCGTAGGATCACCAGACTGGTC
721	LeuValValValAlaValPheValValCysTrpThrProIleHisIlePheIleLeuVal CTGGTGGTGGTGGCAGTCTTCGTCGTCGTGGACTCCCATTCACATATTTCATCCTGGTG
781	GluAlaLeuGlySerThrSerHisSerThrAlaAlaLeuSerSerTyrTyrPheCysIle GAGGCTCTGGGAGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATC
841	AlaLeuGlyTyrThrAsnSerSerLeuAsnProIleLeuTyrAlaPheLeuAspGluAsn GCCTTAGGCTATACCAACAGTAGCCTGAATCCCATTTCTCTACGCCCTTCTTGATGAAAC
901	PheLysArgCysPheArgAspPheCysPheProLeuLysMetNNNMetGluArgNNNSer TTCAAGCGGTGTTCCGGGACTTCTGCTTCCACTGAAGATGAGNATGGAGCGCNAGAGC
961	ThrSerArgValArgAsnThrValGlnAspProAlaTyrLeuArgGluIleAspGlyMet ACTAGCAGAGTCCGAAATACAGTTCAGGATCCTGCTTACCTGAGGGAGATCGATGGGATG
1021	MetAsnLysProValop (SEQ ID NO:12) ATGAATAAACCCAGTATGACTAGTCGTGGA (SEQ ID NO:11)

FIG. 3C

HUMAN
MOUSE

FIG. 4A-1

REPLACEMENT
SHEET

HUMAN	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	Val	Thr	Thr	Thr	Met	
MOUSE	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	Val	Thr	Thr	Thr	Met	
				100					105							110	
HUMAN	Pro	Phe	Gln	Ser	Thr	Val	Tyr	Leu	Met	Asn	Ser	Trp	Pro	Phe	Gly	Asp	
MOUSE	Pro	Phe	Gln	Ser	Ala	Val	Tyr	Leu	Met	Asn	Ser	Trp	Pro	Phe	Gly	Asp	
				115				120								125	
HUMAN	Val	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	
MOUSE	Val	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	
				130			135						140				
HUMAN	Ser	Ile	Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	
MOUSE	Ser	Ile	Phe	Thr	Leu	Thr	Met	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	
				145			150				155					160	
HUMAN	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Leu	Lys	Ala	Lys	
MOUSE	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Leu	Lys	Ala	Lys	
					165			170								175	
UMAN	Ile	Ile	Asn	Ile	Cys	Ile	Trp	Leu	Leu	Ser	Ser	Ser	Val	Gly	Ile	Ser	
MOUSE	Ile	Ile	Asn	Ile	Cys	Ile	Trp	Leu	Leu	Ala	Ser	Ser	Val	Gly	Ile	Ser	
				180						185						190	

FIG. 4A-2

REPLACEMENT
SHEET

HUMAN	Ala	Ile	Val	Leu	Gly	Gly	Thr	Lys	Val	Arg	Glu	Asp	Val	Asp	Val	Ile
MOUSE	Ala	Ile	Val	Leu	Gly	Gly	Thr	Lys	Val	Arg	Glu	Asp	Val	Asp	Val	Ile
			195					200							205	

HUMAN	Glu	Cys	Cys	Leu	Gln	Phe	Pro	Asp	Asp	Asp	Tyr	Ser	Trp	Trp	Asp	Leu
MOUSE	Glu	Cys	Ser	Leu	Gln	Phe	Pro	Asp	Asp	Glu	Tyr	Ser	Trp	Trp	Asp	Leu
			210				215					220				

HUMAN	Phe	Met	Lys	Ile	Cys	Val	Phe	Ile	Phe	Ala	Phe	Val	Ile	Pro	Val	Leu
MOUSE	Phe	Met	Lys	Ile	Cys	Val	Phe	Val	Phe	Ala	Phe	Val	Ile	Pro	Val	Leu
	225					230					235					240

HUMAN	Ile	Ile	Ile	Val	Cys	Tyr	Thr	Leu	Met	Ile	Leu	Arg	Leu	Lys	NNN	Val
MOUSE	Ile	Ile	Ile	Val	Cys	Tyr	Thr	Leu	Met	Ile	Leu	Arg	Leu	Lys	Ser	Val
					245					250					255	

HUMAN	Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	NNN	Asn	Leu	Arg	Arg	Ile
MOUSE	Arg	Leu	Leu	Ser	Gly	Ser	Arg	Glu	Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile
					260					265						270

FIG. 4A-3

HUMAN	Thr	Arg	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe	Val	Val	Cys	Trp	Thr
MOUSE	Thr	Lys	Leu	Val	Leu	Val	Val	Val	Ala	Val	Phe	Ile	Ile	Cys	Trp	Thr
			275				280						285			
HUMAN	Pro	Ile	His	Ile	Phe	Ile	Leu	Val	Glu	Ala	Leu	Gly	Ser	Thr	Ser	His
MOUSE	Pro	Ile	His	Ile	Phe	Ile	Leu	Val	Glu	Ala	Leu	Gly	Ser	Thr	Ser	His
		290					295					300				
HUMAN	Ser	Thr	Ala	Ala	Leu	Ser	Ser	Tyr	Tyr	Phe	Cys	Ile	Ala	Leu	Gly	Tyr
MOUSE	Ser	Thr	Ala	Ala	Leu	Ser	Ser	Tyr	Tyr	Phe	Cys	Ile	Ala	Leu	Gly	Tyr
	305					310					315					320
HUMAN	Thr	Asn	Ser	Ser	Leu	Asn	Pro	Ile	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn
MOUSE	Thr	Asn	Ser	Ser	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn
						325					330					335

FIG. 4B-1

HUMAN	Phe	Lys	Arg	Cys	Phe	Arg	Asp	Phe	Cys	Phe	Pro	Leu	Lys	Met	NNN	Met
MOUSE	Phe	Lys	Arg	Cys	Phe	Arg	Asp	Phe	Cys	Phe	Pro	Ile	Lys	Met	Arg	Met
																350
																345
																340

HUMAN	Glu	Arg	NNN	Ser	Thr	Ser	Arg	Val	Arg	Asn	Thr	Val	Gln	Asp	Pro	Ala
MOUSE	Glu	Arg	Gln	Ser	Thr	Asn	Arg	Val	Arg	Asn	Thr	Val	Gln	Asp	Pro	Ala
																365
																360
																355

HUMAN	Tyr	Leu	Arg	Glu	Ile	Asp	Gly	Met	Met	Asn	Lys	Pro	Val		(SEQ ID NO:12)
MOUSE	:	Ser	Met	Arg	Asp	Val	Gly	Gly	Met	Asn	Lys	Pro	Val		(SEQ ID NO:2)
															380
															375
															370

FIG. 4B-2

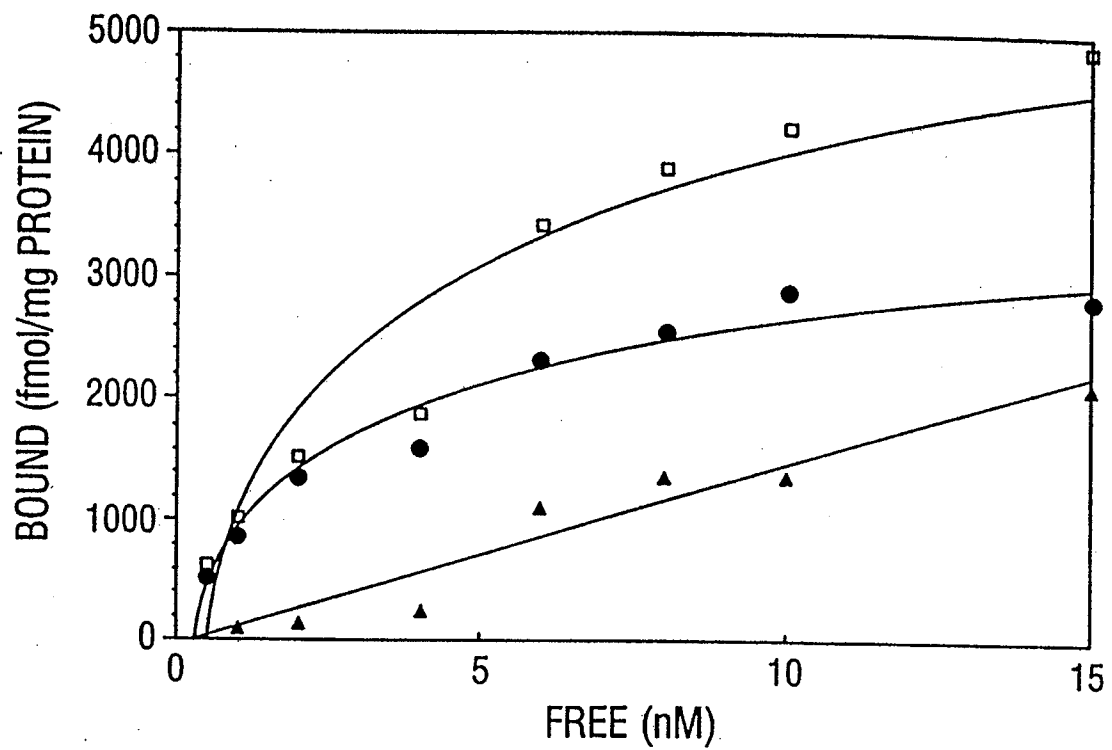


FIG. 5A

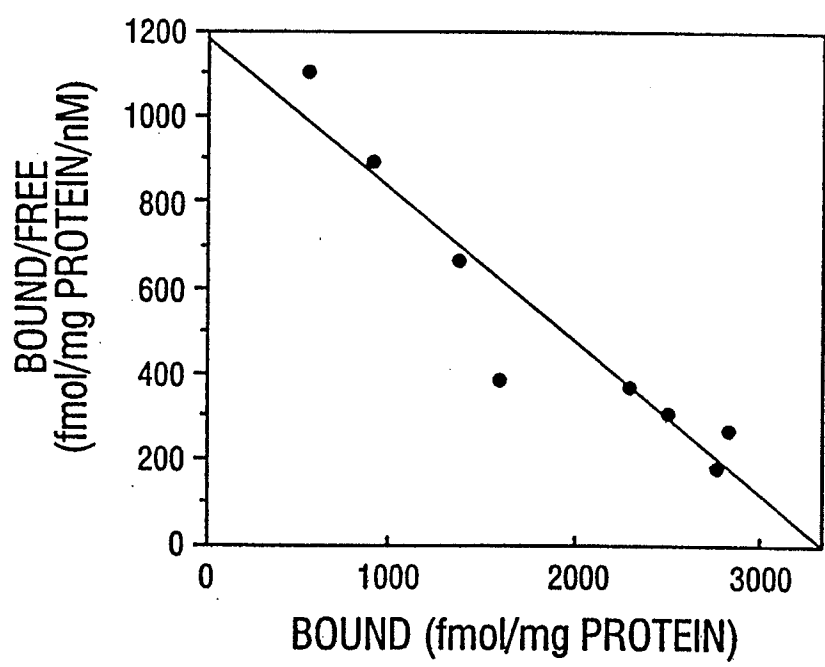


FIG. 5B

REPLACEMENT
SHEET

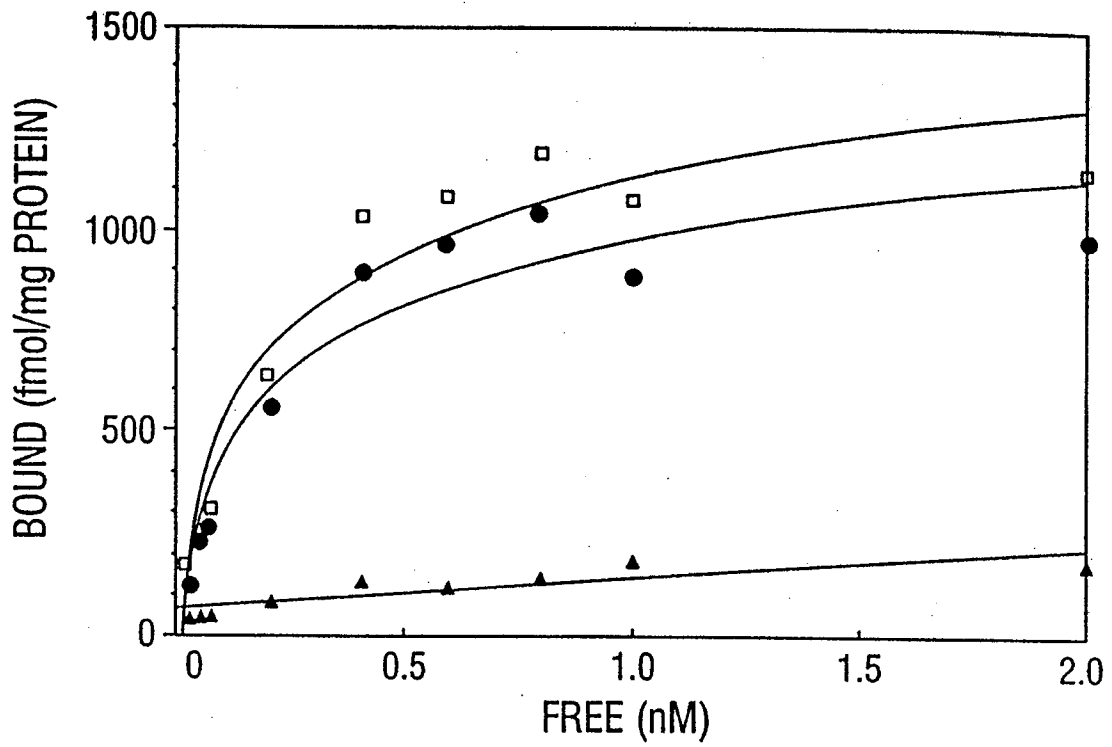


FIG. 5C

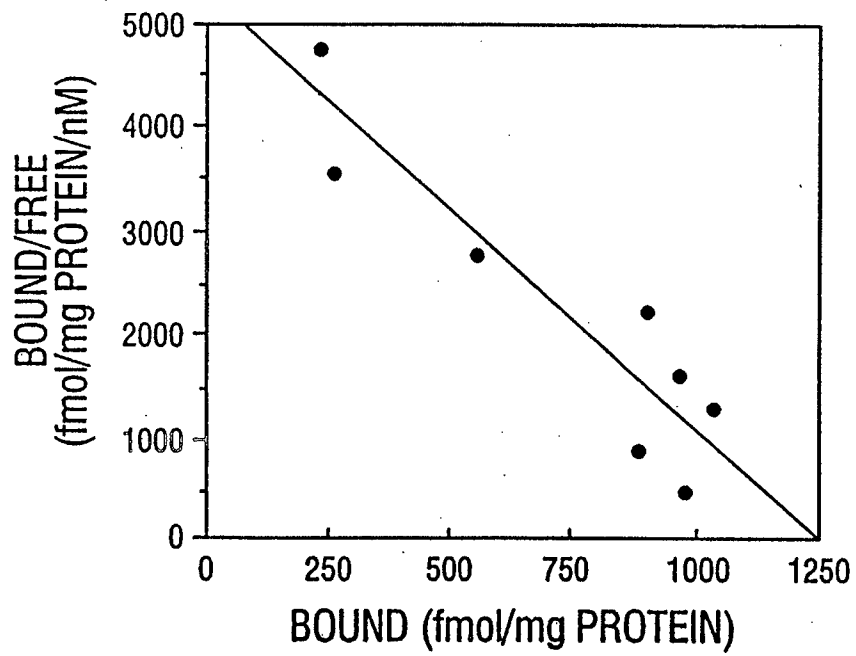


FIG. 5D

REPLACEMENT
SHEET

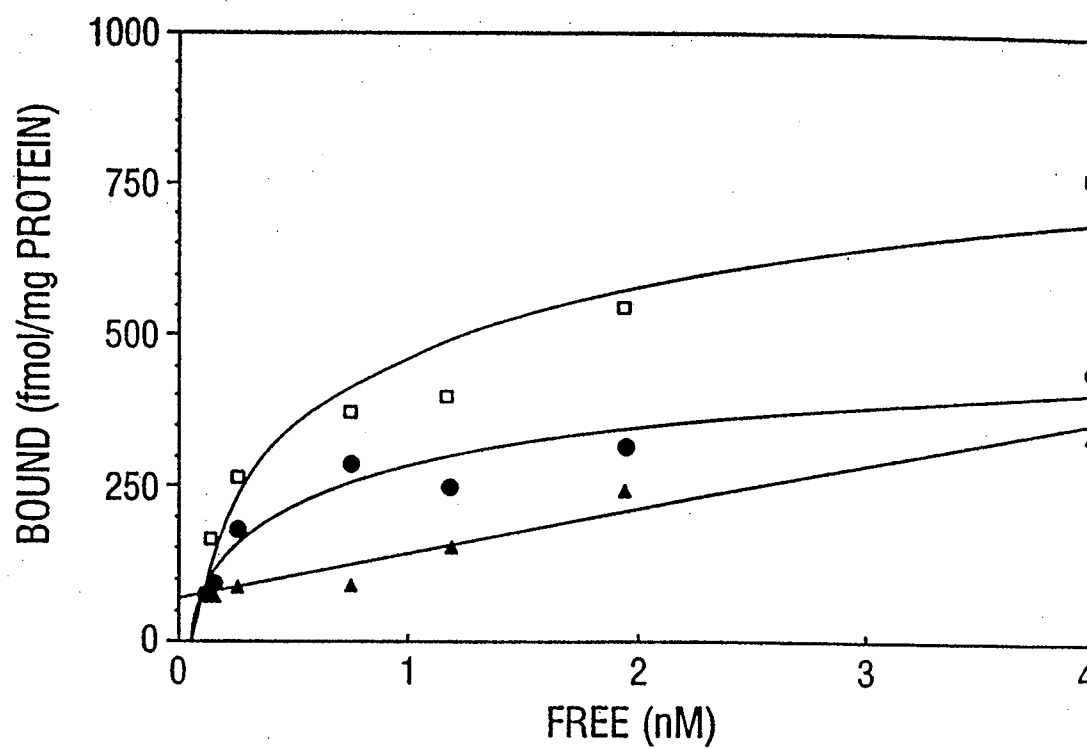


FIG. 5E

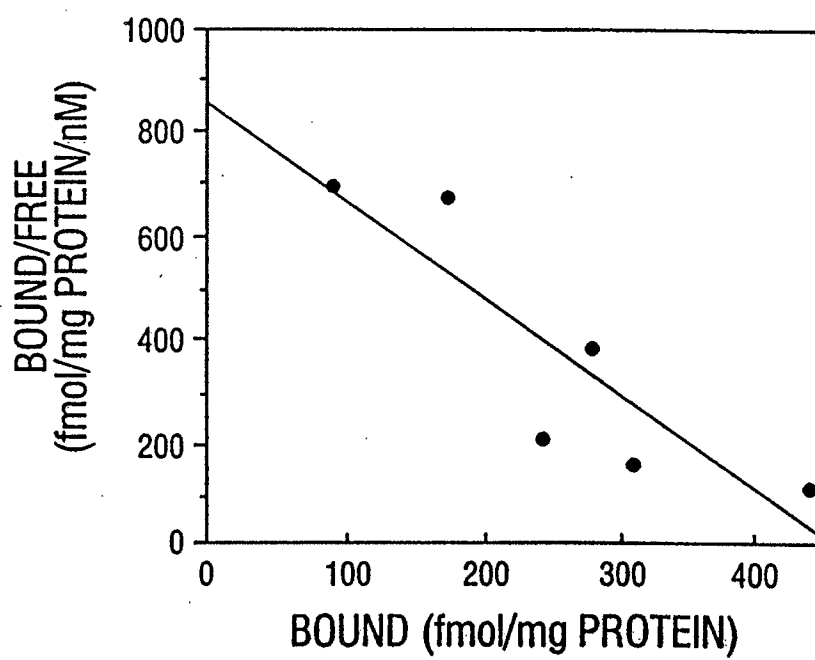


FIG. 5F

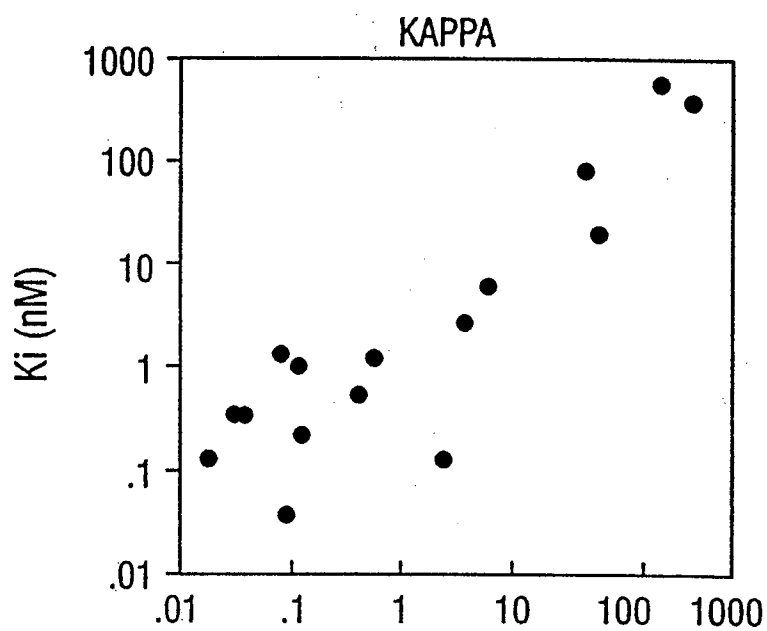


FIG. 6A

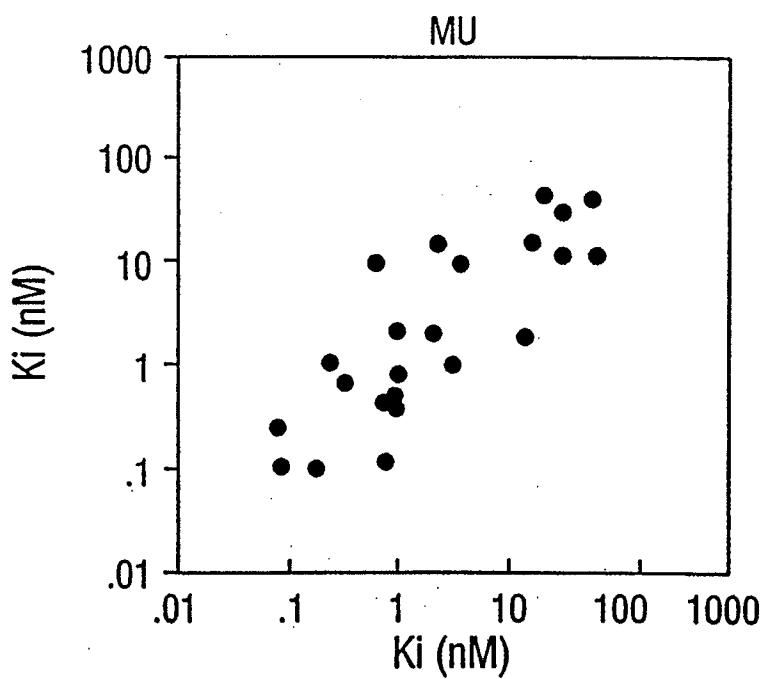


FIG. 6B

REPLACEMENT
SHEET

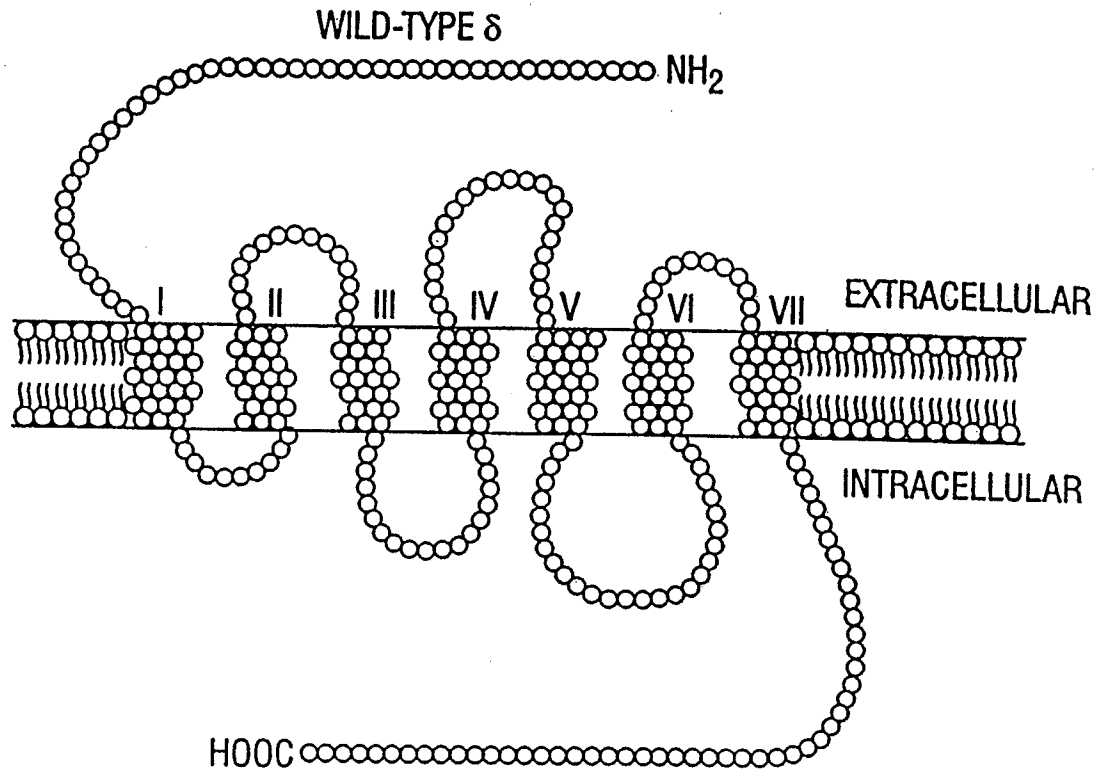


FIG. 7A

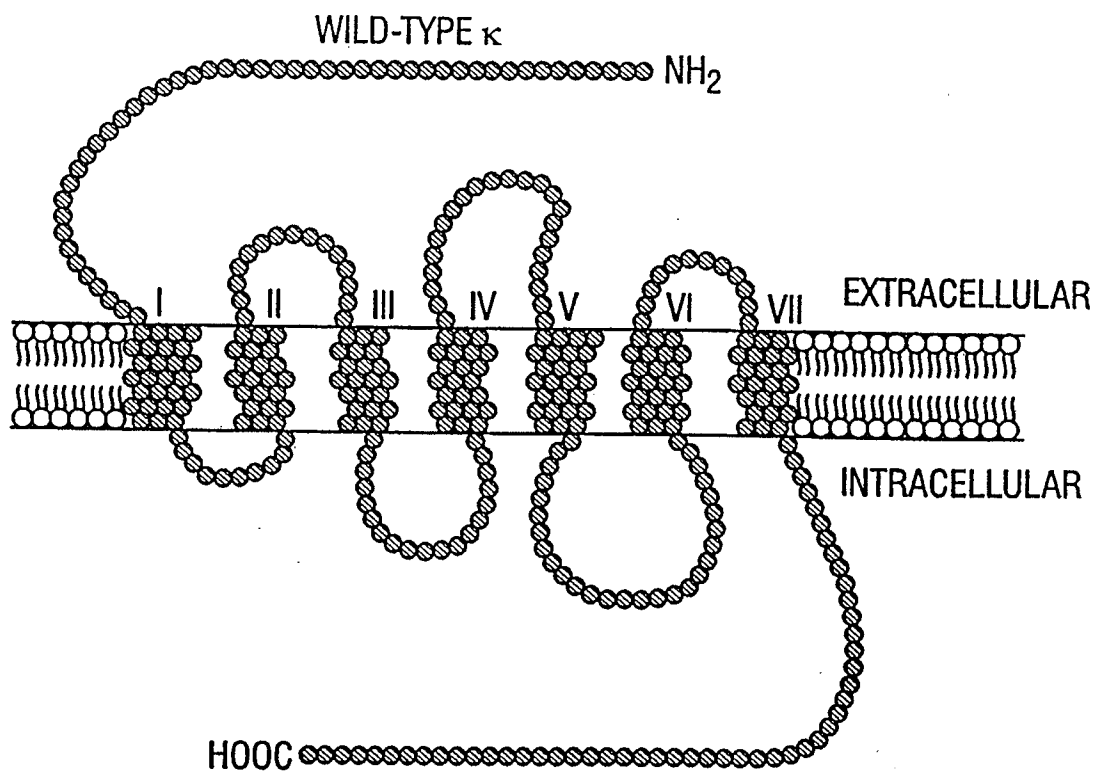


FIG. 7B

REPLACEMENT
SHEET

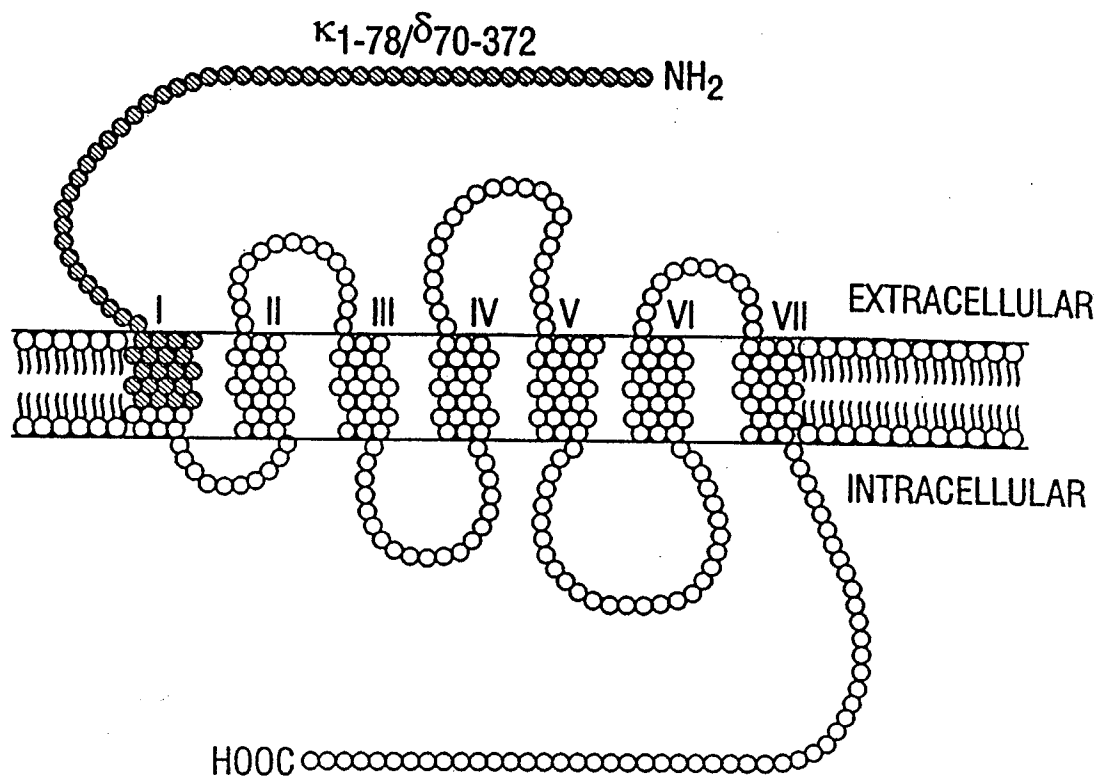


FIG. 7C

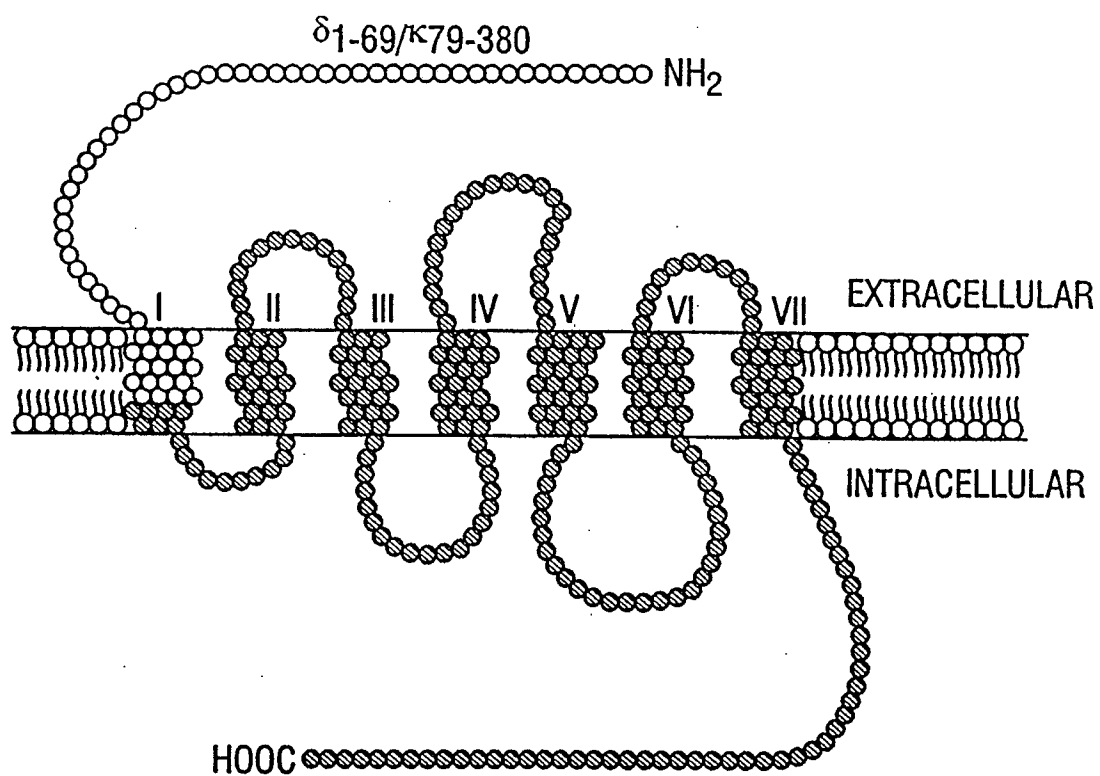


FIG. 7D

REPLACEMENT
SHEET

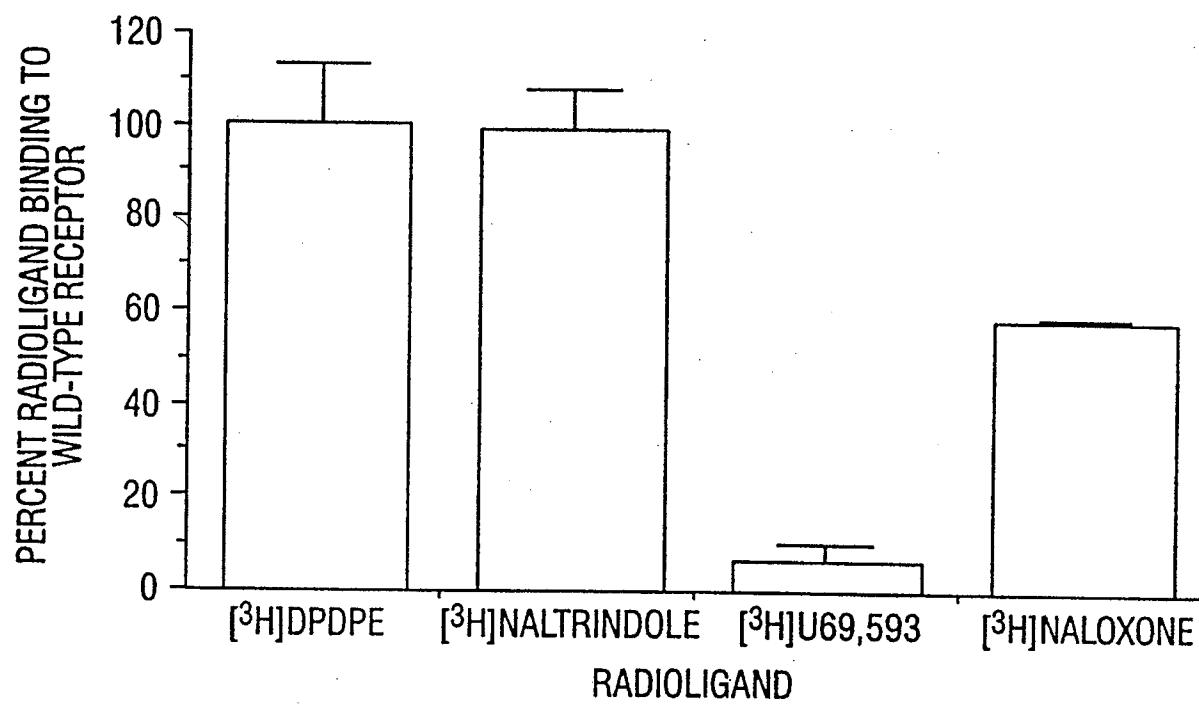


FIG. 8

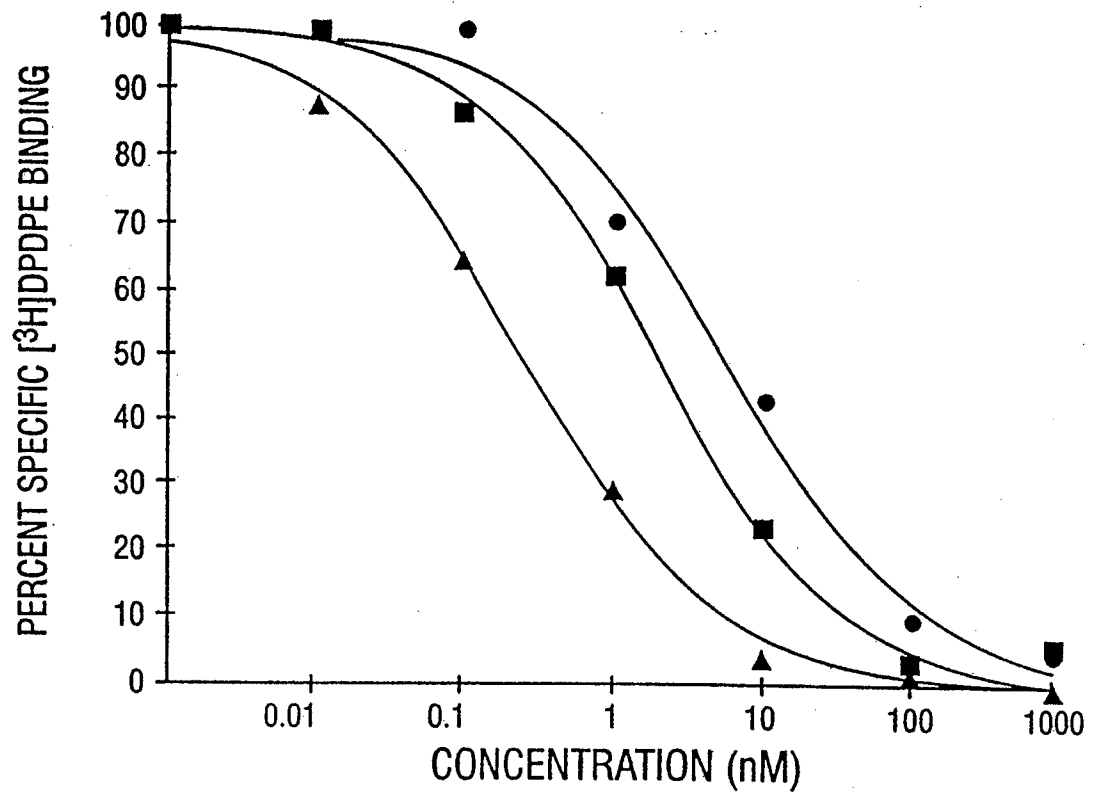


FIG. 9A

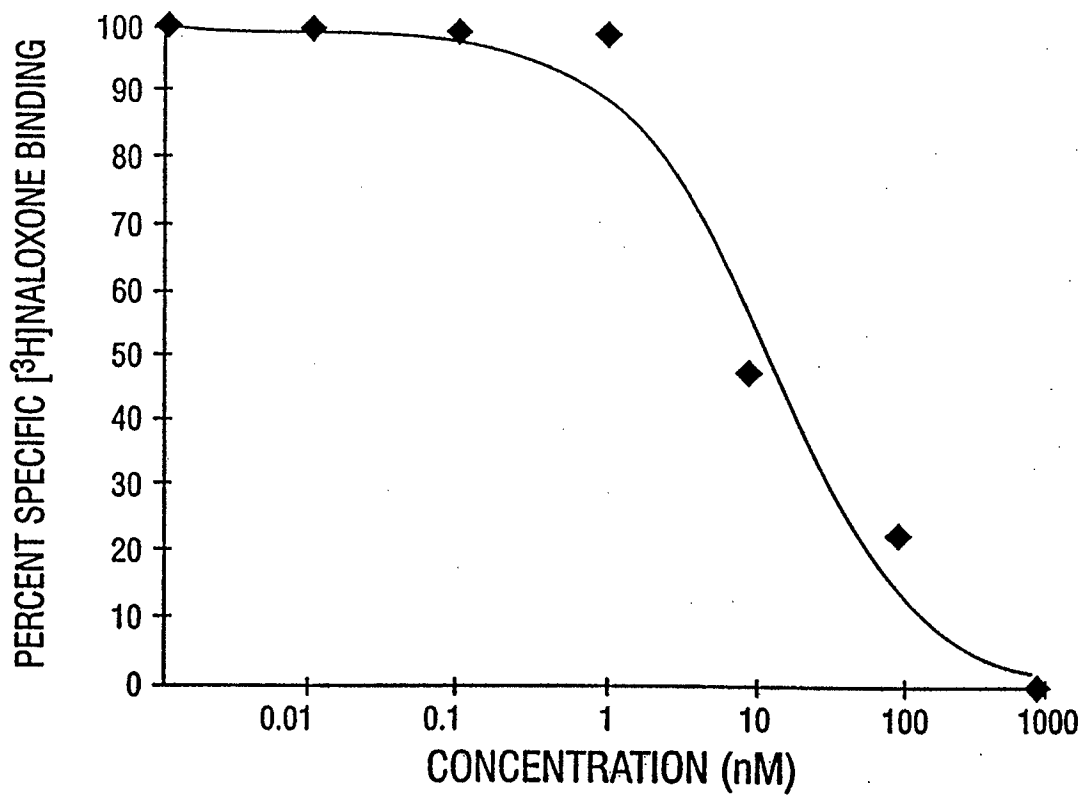


FIG. 9B

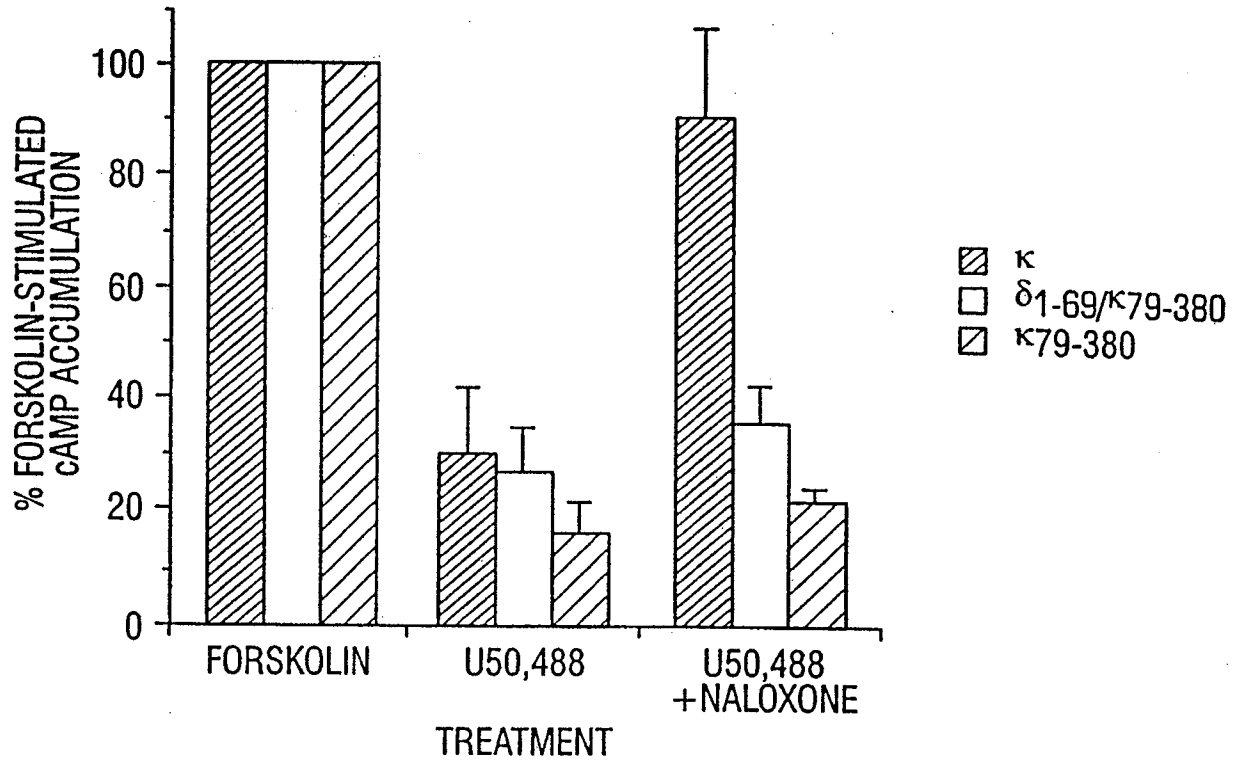


FIG. 10A

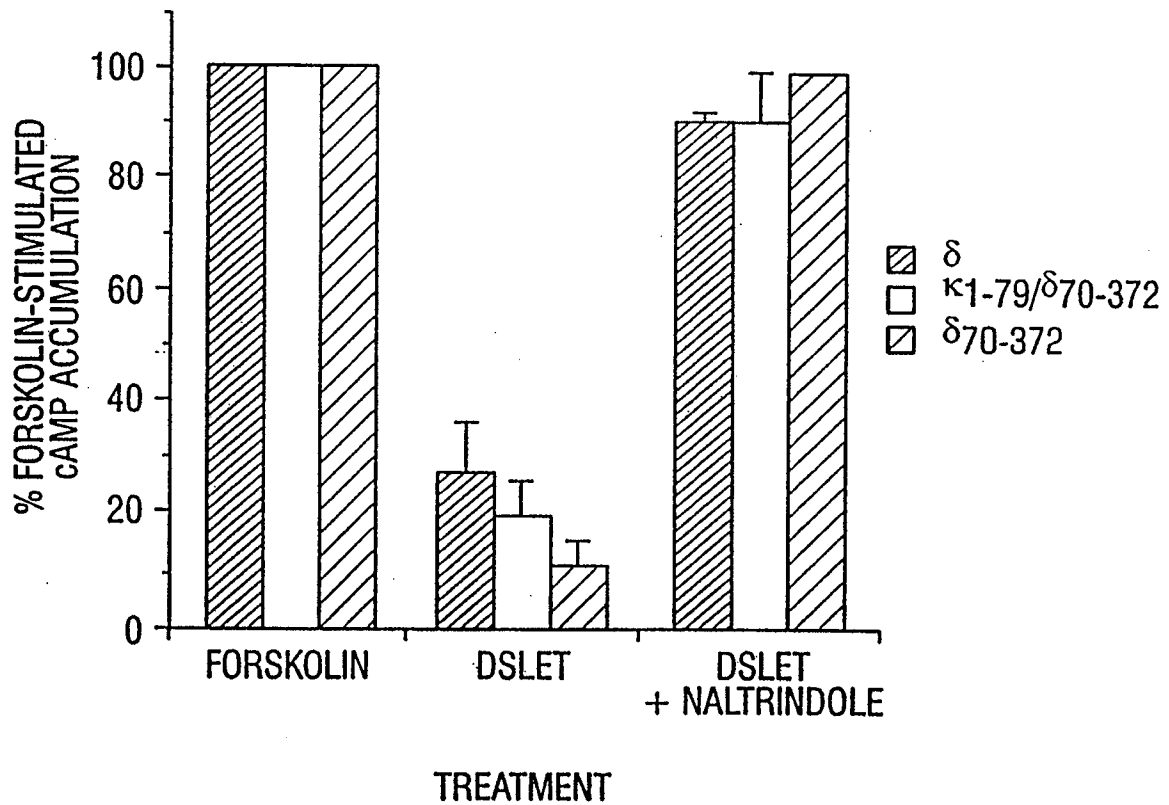


FIG. 10B

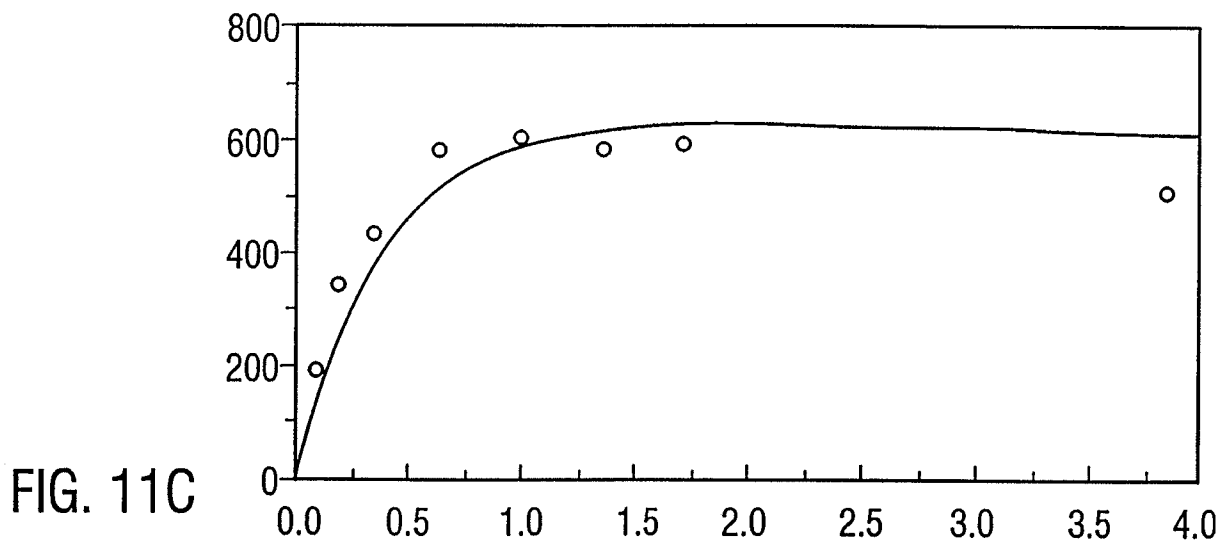
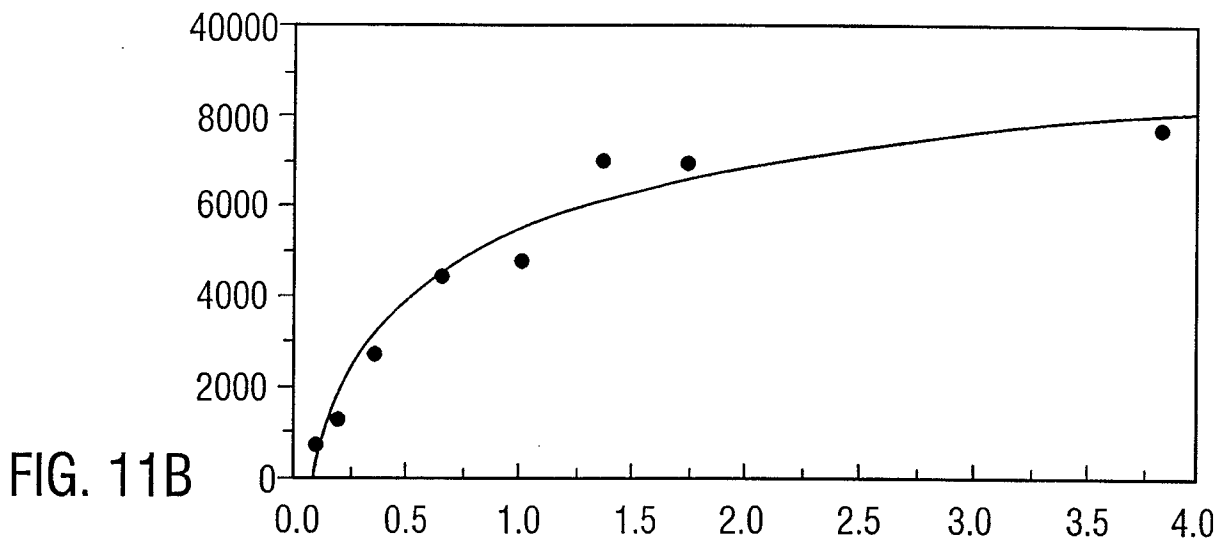
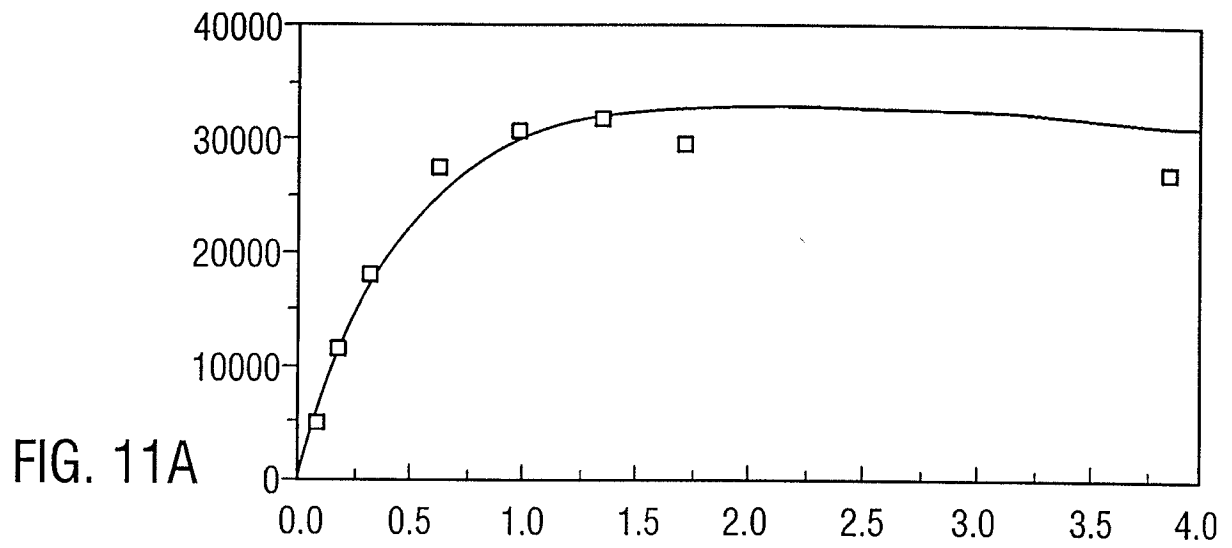


FIG. 12A

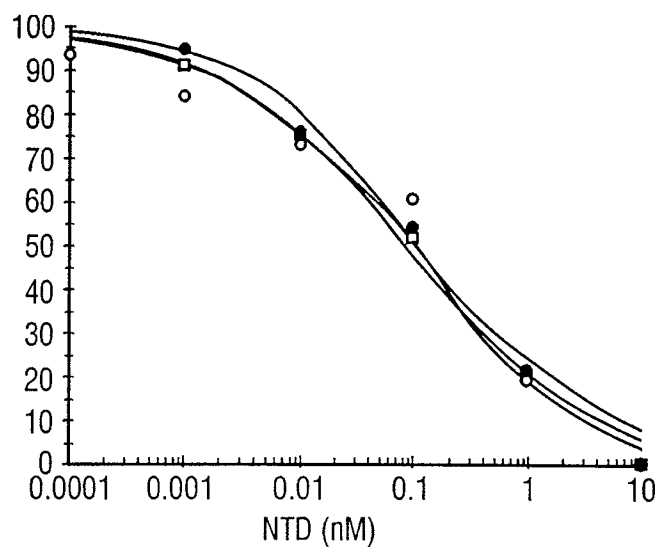


FIG. 12B

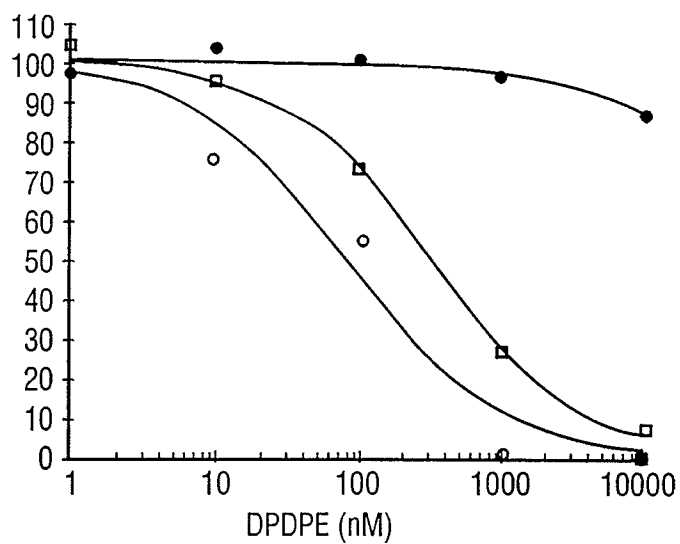
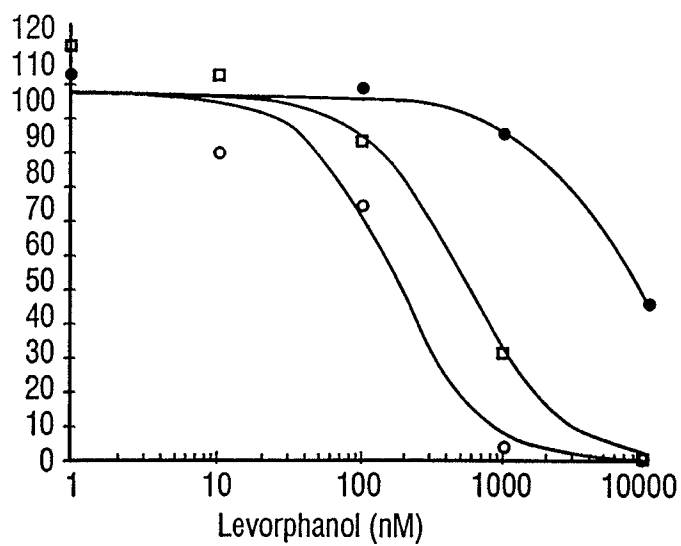


FIG. 12C



REPLACEMENT
SHEET

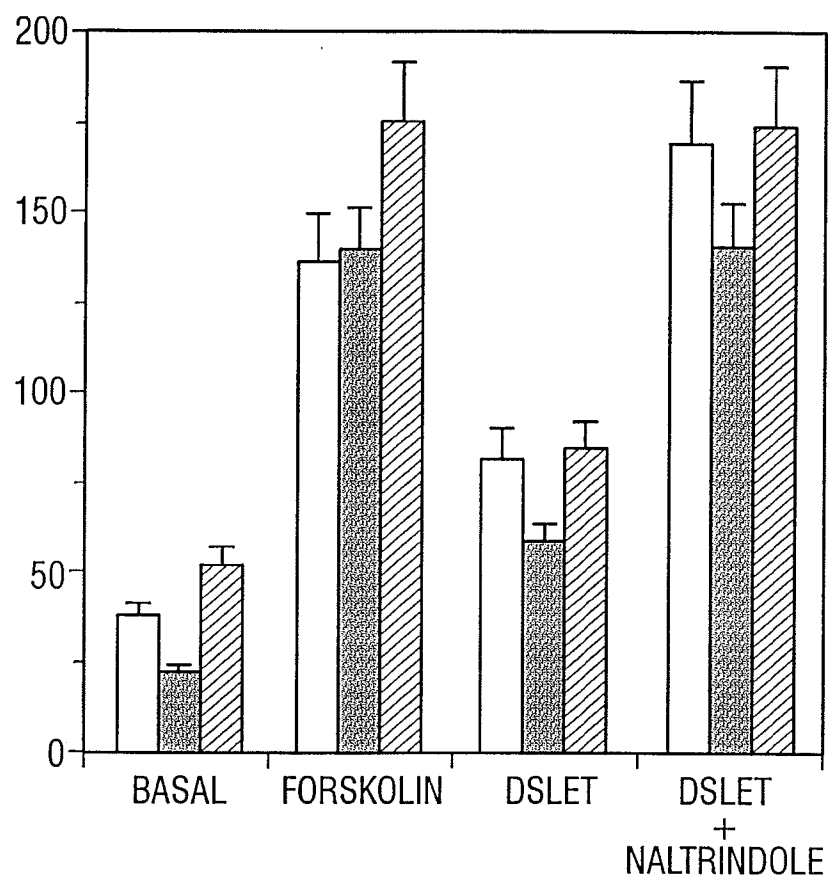


FIG. 13

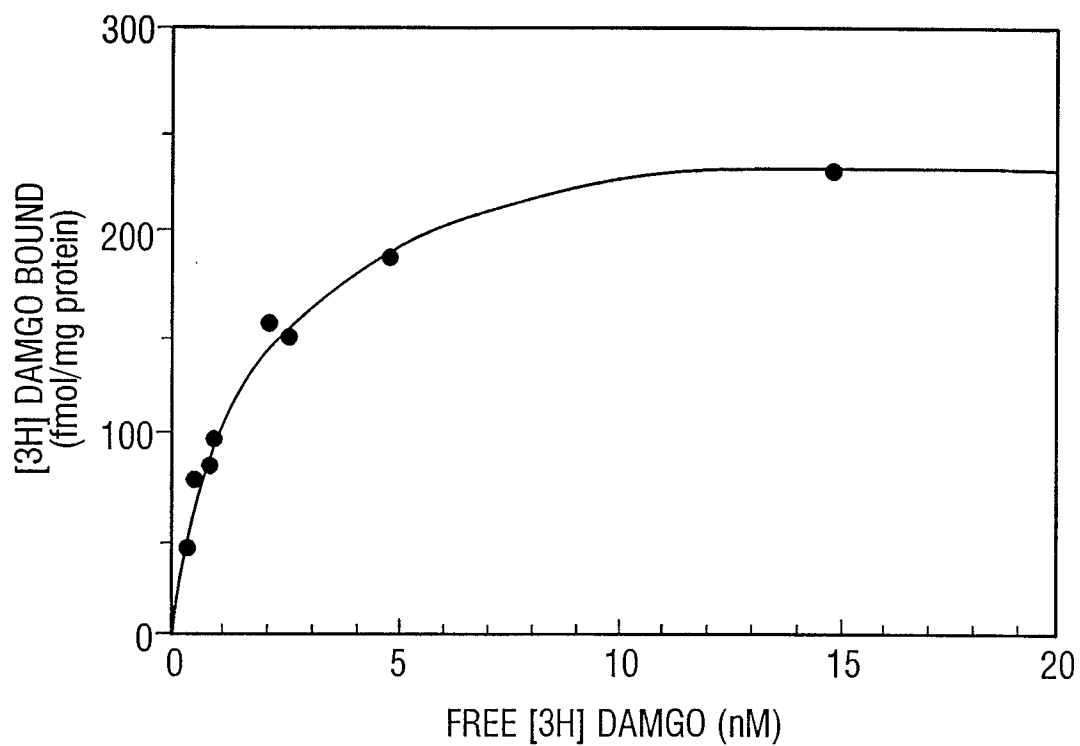


FIG. 14A

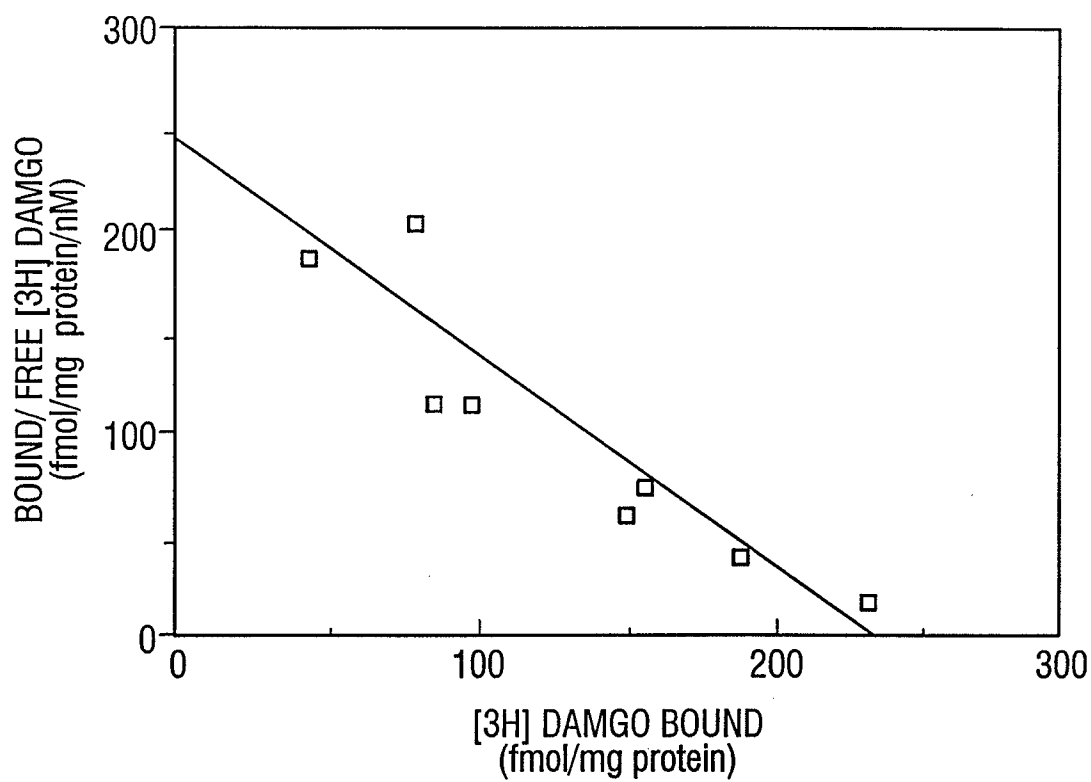


FIG. 14B

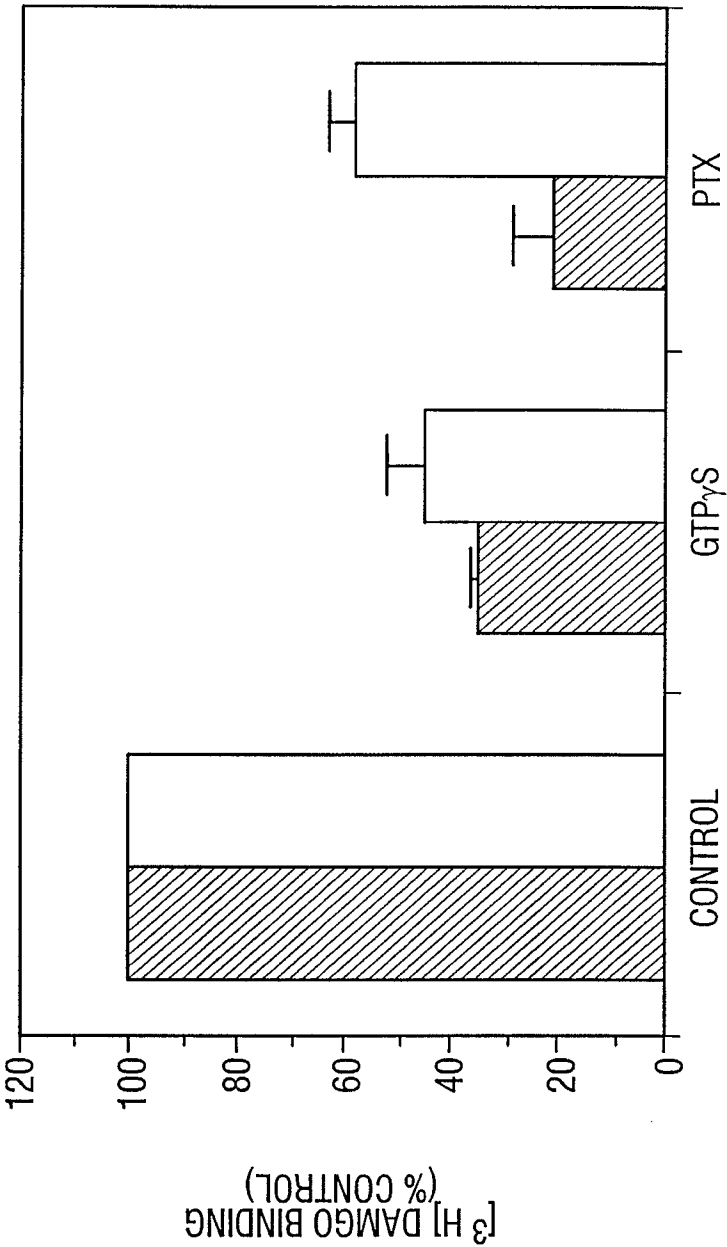


FIG. 15

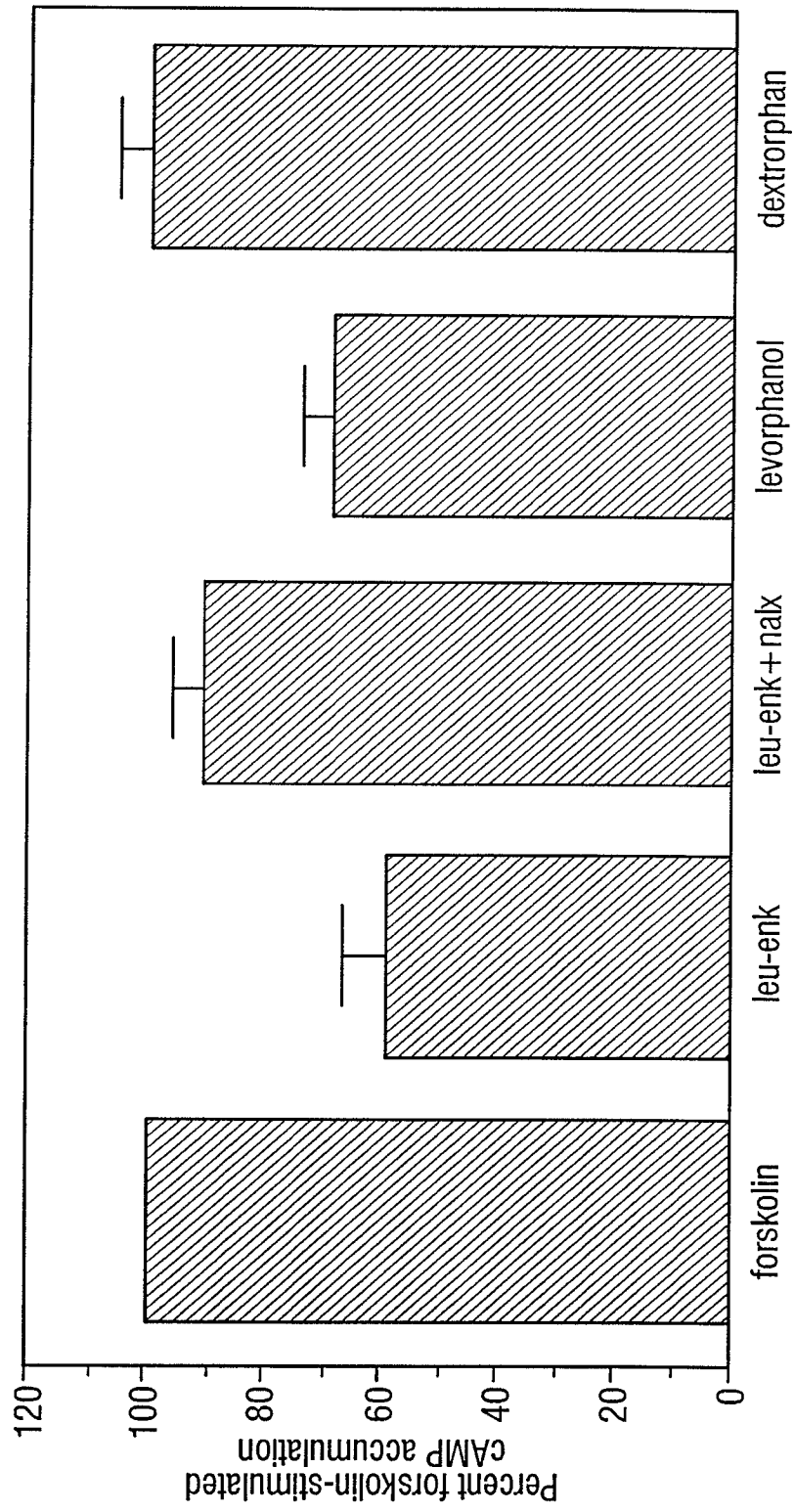


FIG. 16

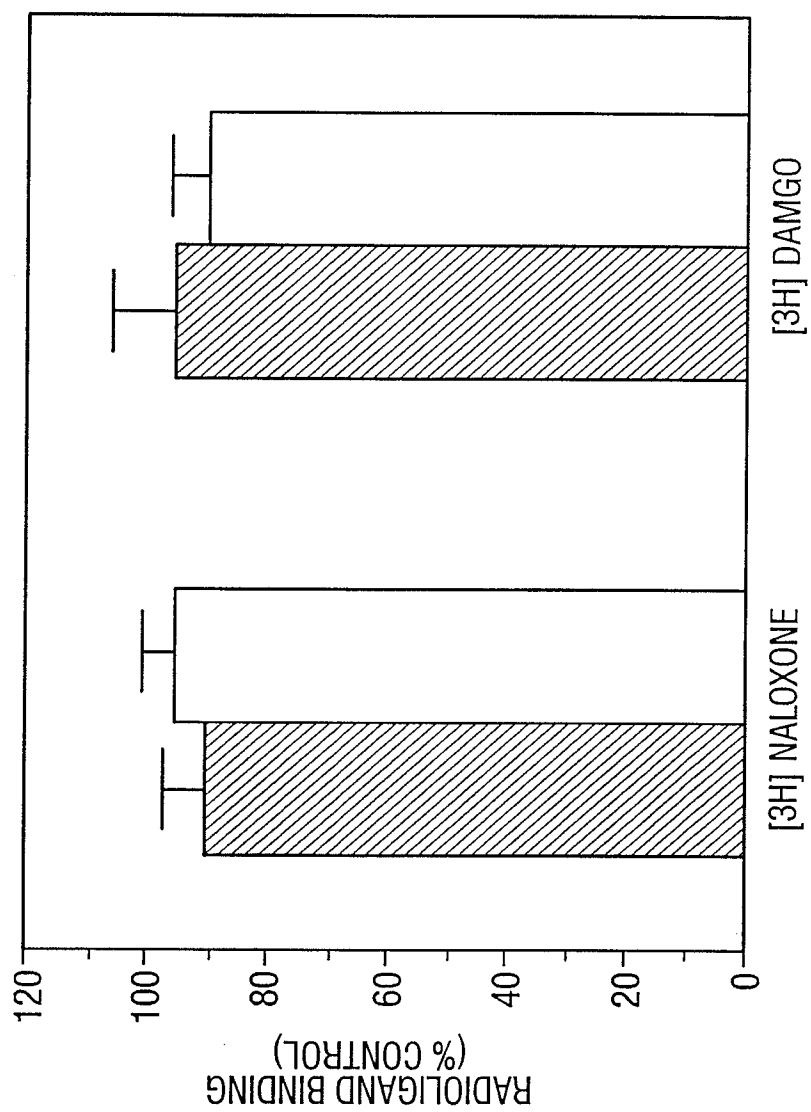


FIG. 17

**REPLACEMENT
SHEET**

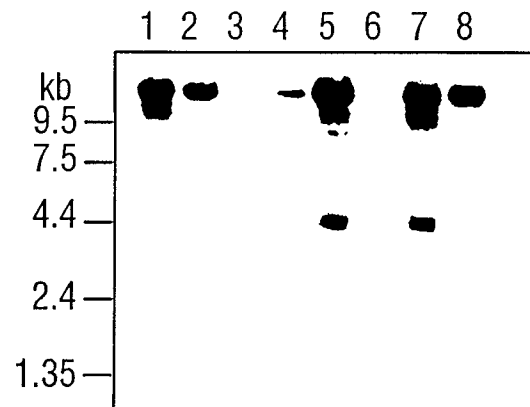


FIG. 18